

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/784,102A

Source: IFW/6

Date Processed by STIC: 9/26/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 09/26/2005

PATENT APPLICATION: US/10/781,102A

TIME: 10:32:41

Input Set : A:\PC10350B.ST25.txt

Output Set: N:\CRF4\09262005\J781102A.raw

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3 <110> APPLICANT: Pfizer Inc.
4     Fidock, Mark
6 <120> TITLE OF INVENTION: PHOSPHODIESTERASE ENZYMES
8 <130> FILE REFERENCE: PC10350B
10 <140> CURRENT APPLICATION NUMBER: 10/781,102A
11 <141> CURRENT FILING DATE: 2004-02-18
13 <150> PRIOR APPLICATION NUMBER: US 09/663,481
14 <151> PRIOR FILING DATE: 2000-09-15
16 <150> PRIOR APPLICATION NUMBER: UK 9922125.1
17 <151> PRIOR FILING DATE: 1999-09-17
19 <150> PRIOR APPLICATION NUMBER: US 60/177,326
20 <151> PRIOR FILING DATE: 2000-01-20
22 <160> NUMBER OF SEQ ID NOS: 23
24 <170> SOFTWARE: PatentIn version 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 516
28 <212> TYPE: PRT
29 <213> ORGANISM: Homo sapiens
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37 Leu Arg Leu Arg Tyr Met Val Lys Gln Leu Glu Asn Gly Glu Ile Asn
38           20           25           30
41 Ile Glu Glu Leu Lys Lys Asn Leu Glu Tyr Thr Ala Ser Leu Leu Glu
42           35           40           45
45 Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp Thr Glu Asp Glu
46           50           55           60
49 Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu Val Arg Asp Trp
50 65           70           75           80
53 Leu Ala Ser Thr Phe Thr Gln Gln Ala Arg Ala Lys Gly Arg Arg Ala
54           85           90           95
57 Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala Val Gln Ala Gly
58           100          105          110
61 Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr Ser Val Gly Pro
62           115          120          125
65 Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn Leu Asp Leu Trp
66           130          135          140
69 Cys Phe Asp Val Phe Ser Leu Asn Gln Ala Ala Asp Asp His Ala Leu
70 145          150          155          160
73 Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn Leu Ile Ser Arg
74           165          170          175
77 Phe Lys Ile Pro Thr Val Phe Leu Met Ser Phe Leu Asp Ala Leu Glu
78           180          185          190

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82      195      200      205
85 Ala Asp Val Thr Gln Thr Val His Cys Phe Leu Leu Arg Thr Gly Met
86      210      215      220
89 Val His Cys Leu Ser Glu Ile Glu Leu Leu Ala Ile Ile Phe Ala Ala
90 225      230      235      240
93 Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn Ser Phe His Ile
94      245      250      255
97 Gln Thr Lys Ser Glu Cys Ala Ile Val Tyr Asn Asp Arg Ser Val Leu
98      260      265      270
101 Glu Asn His His Ile Ser Ser Val Phe Arg Leu Met Gln Asp Asp Glu
102      275      280      285
105 Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe Val Glu Leu Arg
106      290      295      300
109 Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met Ser Cys His Phe
110 305      310      315      320
113 Gln Gln Val Lys Thr Met Lys Thr Ala Leu Gln Gln Leu Glu Arg Ile
114      325      330      335
117 Asp Lys Pro Lys Ala Leu Ser Leu Leu Leu His Ala Ala Asp Ile Ser
118      340      345      350
121 His Pro Thr Lys Gln Trp Leu Val His Ser Arg Trp Thr Lys Ala Leu
122      355      360      365
125 Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala Glu Leu Gly Leu
126      370      375      380
129 Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu Val Ala Gln Ser
130 385      390      395      400
133 Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr Phe Ser Val Leu
134      405      410      415
137 Thr Asp Val Ala Glu Lys Ser Val Gln Pro Leu Ala Asp Glu Asp Ser
138      420      425      430
141 Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln Pro Ser Leu Asp
142      435      440      445
145 Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser Phe Arg Ser Thr
146      450      455      460
149 Trp Val Lys Arg Ile Gln Glu Asn Lys Gln Lys Trp Lys Glu Arg Ala
150 465      470      475      480
153 Ala Ser Gly Ile Thr Asn Gln Met Ser Ile Asp Glu Leu Ser Pro Cys
154      485      490      495
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158      500      505      510
161 Gly Asn Leu Asp
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165 <210> SEQ ID NO: 2
166 <211> LENGTH: 3091
167 <212> TYPE: DNA
168 <213> ORGANISM: Homo sapiens
170 <400> SEQUENCE: 2
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179	ggagtacaca	gcttctctgc	tgggaagcgt	ctacatagat	gagacacggc	aaatcttgga	300
181	cacggaggac	gagctgcagg	agctgcggtc	agatgccgtg	ccttcggagg	tgcgggactg	360
183	gctggcctcc	accttcaccc	agcaggcccc	ggccaaaggc	cgccgagcag	aggagaagcc	420
185	caagtccga	agcattgtgc	acgctgtgca	ggctgggac	ttcgtggaac	ggatgttccg	480
187	gagaacatac	acctctgtgg	gccccactta	ctctactgcg	gttctcaact	gtctcaagaa	540
189	cctggatctc	tgggtgcttg	atgtcttttc	cttgaaccag	gcagcagatg	acctatgccct	600
191	gaggaccatt	gtttttgagt	tgctgactcg	gcataacctc	atcagccgct	tcaagattcc	660
193	cactgtgttt	ttgatgagtt	tcctggatgc	cttggagaca	ggctatggga	agtacaagaa	720
195	tccttaccac	aaccagatcc	acgcagccga	tgttaccacg	acagtccatt	gcttcttgct	780
197	ccgcacaggg	atggtgcact	gcctgtcgga	gattgagctc	ctggccatca	tctttgctgc	840
199	agctatccat	gattatgagc	acacgggcac	taccaacagc	ttccacatcc	agaccaagtc	900
201	agaatgtgcc	atcgtgtaca	atgatcgttc	agtgtcggag	aatcaccaca	tcagctctgt	960
203	tttccgattg	atgcaggatg	atgagatgaa	cattttcacc	aacctcacca	aggatgagtt	1020
205	tgtagaactc	cgagccctgg	tcattgagat	gggtgtggcc	acagacatgt	cctgccattt	1080
207	ccagcaagtg	aagaccatga	agacagcctt	gcaacagctg	gagaggattg	acaagcccaa	1140
209	ggccctgtct	ctactgctcc	atgctgctga	catcagccac	ccaaccaagc	agtggttggt	1200
211	ccacagccgt	tggaccaagg	ccctcatgga	ggaattcttc	cgtcagggtg	acaaggaggc	1260
213	agagttgggc	ctgccctttt	ctccactctg	tgaaccgact	tccactctag	tggcacagtc	1320
215	tcagataggg	ttcatcgact	tcattgtgga	gccacatttc	tctgtgctga	ctgacgtggc	1380
217	agagaagagt	gttcagcccc	tggcggatga	ggactccaag	tctaaaaacc	agcccagctt	1440
219	tcagtggcgc	cagccctctc	tggatgtgga	agtgggagac	cccaaccctg	atgtggtcag	1500
221	ctttcgttcc	acctgggtca	agcgcattca	ggagaataag	cagaaatgga	aggaacgggc	1560
223	agcaagtggc	atcaccaacc	agatgtccat	tgacgagctg	tccccctgtg	aagaagaggc	1620
225	ccccccatcc	cctgccgaag	atgaacacaa	ccagaatggg	aatctggatt	agccctgggg	1680
227	ctggccccag	tcttcattga	gtccaaagtg	tttgatgtca	tcagcaccat	ccatcaggac	1740
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231	aatgcccaga	gatttggggg	tggggaaagg	gccccctccc	acctgacacc	cactgggggtg	1860
233	cactttaatg	ttccggcagc	aagactgggg	aacttcaggc	tcccagtggg	cactgtgccc	1920
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237	tggaggcttc	ccagggcctt	ggggaagggg	cagagatgcc	agccccctgg	gacctcccc	2040
239	atcctttttg	ctccaagtt	tctaagcaat	acattttggg	ggttccctca	gccccccacc	2100
241	ccagatctta	gctggcaggt	ctgggtgccc	cttttccctc	cctgggaagg	gctggaatag	2160
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253	cctttgctc	cttctctctc	cctggggctg	ggaggctcca	tccgaccaat	gtctgtaaag	2520
255	tgctttgagg	atctccccag	caaagcacct	tcagaatgta	tcgacaccag	ctgggttagg	2580
257	gtcaagggtg	cctggggagg	gtgagtaatc	ctgcattgct	aaaagagagg	gtctgtcccc	2640
259	tcctctccac	gtcccagaac	tggcccagct	gcaggcacta	agaagctcct	ccccctgagac	2700
261	aagtgagggg	tagtcggtga	aaggcagatg	gacaaggggc	tcagggtctg	tgcttctctg	2760
263	tcctctggag	agaaccacag	caggcgcggt	gcccccttct	ctcctcaggc	tcctccttgc	2820
265	ccccaccttg	ccccaggaaa	ggccaaagtc	cagggtgactg	ccctccttct	ttcttgtaaa	2880
267	taccaaccat	gcatttgtac	agtgggcccct	gttcatgcga	aatccacatc	catggtctcc	2940
269	tagacctgct	acctggttac	ttccacccta	ccccaccccg	agaagggcag	agacgcagtg	3000
271	gactcacccc	tgcctttggt	ttcccagacc	cctgctatag	ccagagaaca	ataaagaagg	3060

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273 gagaccagga aaaaaaaaaa aaaaaaaaaa a                                     3091
276 <210> SEQ ID NO: 3
277 <211> LENGTH: 536
278 <212> TYPE: PRT
279 <213> ORGANISM: Homo sapiens
281 <400> SEQUENCE: 3
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284 1          5          10          15
287 Cys Pro Ser Pro Leu Glu Leu Lys Ser Ala Pro Ser Lys Lys Met Trp
288          20          25          30
291 Ile Lys Leu Arg Ser Leu Leu Arg Tyr Met Val Lys Gln Leu Glu Asn
292          35          40          45
295 Gly Glu Ile Asn Ile Glu Glu Leu Lys Lys Asn Leu Glu Tyr Thr Ala
296          50          55          60
299 Ser Leu Leu Glu Ala Val Tyr Ile Asp Glu Thr Arg Gln Ile Leu Asp
300 65          70          75          80
303 Thr Glu Asp Glu Leu Gln Glu Leu Arg Ser Asp Ala Val Pro Ser Glu
304          85          90          95
307 Val Arg Asp Trp Leu Ala Ser Thr Phe Thr Gln Gln Ala Arg Ala Lys
308          100         105         110
311 Gly Arg Arg Ala Glu Glu Lys Pro Lys Phe Arg Ser Ile Val His Ala
312          115         120         125
315 Val Gln Ala Gly Ile Phe Val Glu Arg Met Phe Arg Arg Thr Tyr Thr
316          130         135         140
319 Ser Val Gly Pro Thr Tyr Ser Thr Ala Val Leu Asn Cys Leu Lys Asn
320 145         150         155         160
323 Leu Asp Leu Trp Cys Phe Asp Val Phe Ser Leu Asn Gln Ala Ala Asp
324          165         170         175
327 Asp His Ala Leu Arg Thr Ile Val Phe Glu Leu Leu Thr Arg His Asn
328          180         185         190
331 Leu Ile Ser Arg Phe Lys Ile Pro Thr Val Phe Leu Met Ser Phe Leu
332          195         200         205
335 Asp Ala Leu Glu Thr Gly Tyr Gly Lys Tyr Lys Asn Pro Tyr His Asn
336          210         215         220
339 Gln Ile His Ala Ala Asp Val Thr Gln Thr Val His Cys Phe Leu Leu
340 225         230         235         240
343 Arg Thr Gly Met Val His Cys Leu Ser Glu Ile Glu Leu Leu Ala Ile
344          245         250         255
347 Ile Phe Ala Ala Ala Ile His Asp Tyr Glu His Thr Gly Thr Thr Asn
348          260         265         270
351 Ser Phe His Ile Gln Thr Lys Ser Glu Cys Ala Ile Val Tyr Asn Asp
352          275         280         285
355 Arg Ser Val Leu Glu Asn His His Ile Ser Ser Val Phe Arg Leu Met
356          290         295         300
359 Gln Asp Asp Glu Met Asn Ile Phe Ile Asn Leu Thr Lys Asp Glu Phe
360 305         310         315         320
363 Val Glu Leu Arg Ala Leu Val Ile Glu Met Val Leu Ala Thr Asp Met
364          325         330         335
367 Ser Cys His Phe Gln Gln Val Lys Thr Met Lys Thr Ala Leu Gln Gln

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368          340          345          350
371 Leu Glu Arg Ile Asp Lys Pro Lys Ala Leu Ser Leu Leu Leu His Ala
372          355          360          365
375 Ala Asp Ile Ser His Pro Thr Lys Gln Trp Leu Val His Ser Arg Trp
376          370          375          380
379 Thr Lys Ala Leu Met Glu Glu Phe Phe Arg Gln Gly Asp Lys Glu Ala
380 385          390          395          400
383 Glu Leu Gly Leu Pro Phe Ser Pro Leu Cys Asp Arg Thr Ser Thr Leu
384          405          410          415
387 Val Ala Gln Ser Gln Ile Gly Phe Ile Asp Phe Ile Val Glu Pro Thr
388          420          425          430
391 Phe Ser Val Leu Thr Asp Val Ala Glu Lys Ser Val Gln Pro Leu Ala
392          435          440          445
395 Asp Glu Asp Ser Lys Ser Lys Asn Gln Pro Ser Phe Gln Trp Arg Gln
396          450          455          460
399 Pro Ser Leu Asp Val Glu Val Gly Asp Pro Asn Pro Asp Val Val Ser
400 465          470          475          480
403 Phe Arg Ser Thr Trp Val Lys Arg Ile Gln Glu Asn Lys Gln Lys Trp
404          485          490          495
407 Lys Glu Arg Ala Ala Ser Gly Ile Thr Asn Gln Met Ser Ile Asp Glu
408          500          505          510
411 Leu Ser Pro Cys Glu Glu Glu Ala Pro Pro Ser Pro Ala Glu Asp Glu
412          515          520          525
415 His Asn Gln Asn Gly Asn Leu Asp
416          530          535
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420 <211> LENGTH: 3112
421 <212> TYPE: DNA
422 <213> ORGANISM: Homo sapiens
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429 ggagtcggat tgcccgtcac cctggagct gaagtcagcc ccagcaaga agatgtggat      180
431 taagcttcgg tctctgctgc gctacatggg gaagcagttg gagaatgggg agataaacat      240
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435 tgagacacgg caaatcttgg acacggagga cgagctgcag gagctgcggt cagatgccgt      360
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445 ggcagcagat gaccatgcc tgaaggacct tgtttttgag ttgctgactc ggcataacct      660
447 catcagccgc ttcaagattc ccactgtgtt tttgatgagt ttcttgatg ccttggagac      720
449 aggctatggg aagtacaaga atccttacca caaccagatc cacgcagccg atgttaccca      780
451 gacagtccat tgcttcttgc tccgcacagg gatggtgcac tgcctgtcgg agattgagct      840
453 cctggccatc atcttttctg cagctatcca tgattatgag cacacgggca ctaccaacag      900
455 cttccacatc cagaccaagt cagaatgtgc catcgtgtac aatgatcggt cagtgtctga      960
457 gaatcaccac atcagctctg ttttccgatt gatgcaggat gatgagatga acattttcat      1020
459 caacctcacc aaggatgagt ttgtagaact ccgagccctg gtcattgaga tgggtgttggc      1080
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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 09/26/2005  
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Input Set : A:\PC10350B.ST25.txt  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:14,15,16,17,18,19,20,21

**VERIFICATION SUMMARY**

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